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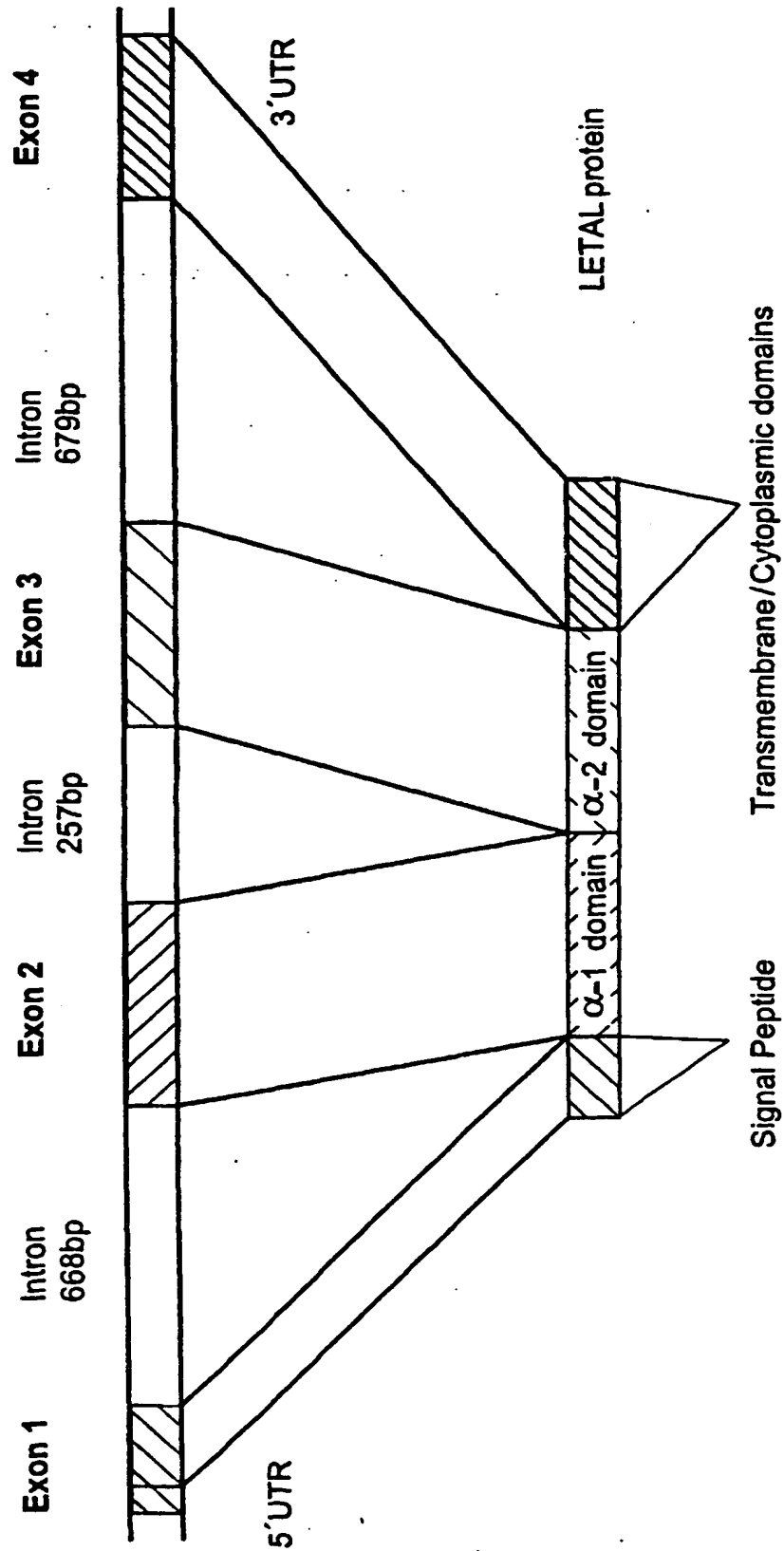


Fig. 1A

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	-----Signal Peptide-----	
ULBP1	MAAAASPALLCLPLL-HLLSGWSRAGWV DTHCLCYDFFITTPKSRPEPQWCEVQGLVDER	
ULBP2	MAAAAATKILLCLPLL-LLLSGWSRAGRA DPHSLCYDITVIPKFRPGPRWCAVQGGQVDEK	
ULBP3	MAAAAAPAILPRLAIPYLLPFDWSGTGRA DAHSLWYNFTIIHLPRHGQQWCEVQSQVDQK	
Letal	-MRRISLTSSPVRLLLFLLLLLIALEIMV GHSLSLCEFNFTIKSLSRPGQFWCEAQVFLNKN	
	----- α -1 domain-----	
ULBP1	PFLHYDCVNHKAKAFASLGKKVNVTKTMEEQTETLRDVVDFFKRGQLLDIQVENLIPIE PL	
ULBP2	TEFLHYDCGNKTVTPVSPPLGKKLVNVTAMKAQNPVLRREVVDIILTEQLLRDIQLENYTPKE PL	
ULBP3	NFLSYDCGSDKVLSMGHLEEQLYATDAWKGQLEMLREVVGQRLRLLELADTELEDFTPSG PL	
Letal	LFLQYNSDNNMVKPLGLLGKKVYATSTWGETQTLEGEVGRDLRMLLCDIKPQIKTS-D PS	
	----- α -2 domain-----	
ULBP1	TLQARMSCHEAHGHGRGSWQFLFNGQKFFLLEDSENRRKWTALHPGAKKMTKWKENNRDVT	
ULBP2	TLQARMSCFEQKAEHGHSSGSWQFSFDGQIFLLEDSEKRMWTTVHPGARMKKEKWKENDKVVA	
ULBP3	TLQVRMSCFECEADGYIRGSWQFSFDGRKFFLLEDSENRRKWTVVHAGARRMKKEKWKDSGLT	
Letal	TLQVEVMFCQREAEERCTGASWQFATNGEKSLLLEDAMNMTWTVINHEASIKETWKKDRGLE	

ULBP1	MFFQKISLGDCKMWLEEFELMYWEQMLDPT K-----PPSLAPGTTQPKAMATT LSPWSLII	
ULBP2	MSFHYFSGMGDCIGWLEDFLMGMDSTLEPS AG--APLAMSSGTTQLRATAATT LILCCLLII	
ULBP3	TFFKMWVSMRDCSKSWLRDFLMHRKKRLEPT A----PPTMAPGLAQPKAIAATT LSPWSFLII	
Letal	KYFERKLSKGDCHWLRREFLGHWEAMPEPT VSPVNASDIHWSSSSSLPDRWII LGAFILVVL	

ULBP1	FLCFILAGR-----	
ULBP2	LPCFILPGI-----	
ULBP3	L-CFILPGI-----	
Letal	MGIVLICVWW QNGEWQAGLWPLRTS	

Fig. 1B

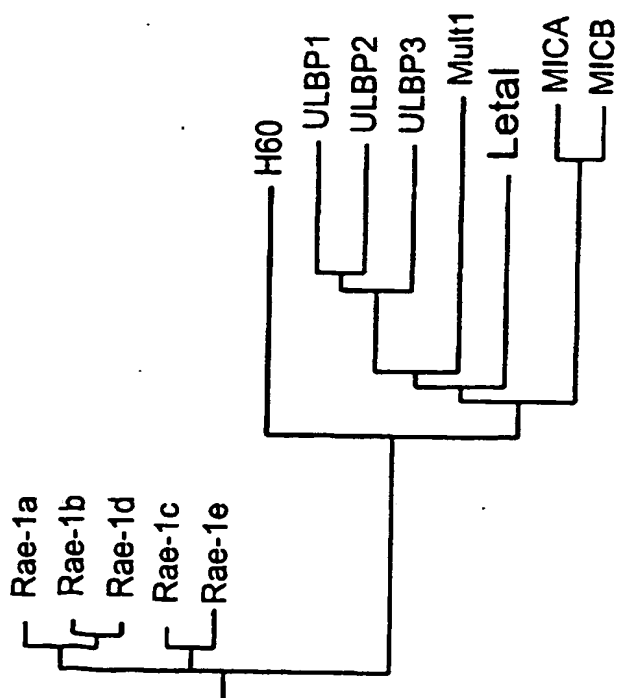
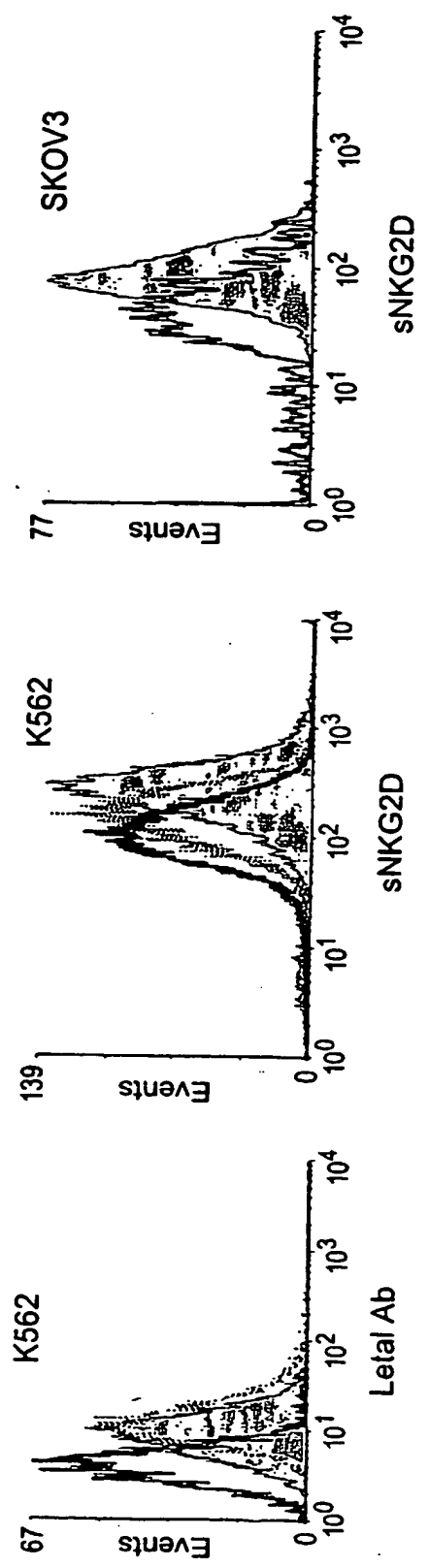


Fig. 1C

Fig. 1D



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Exon 1

ACCATACAGTGAGGGTGAATGTGTACACGCCCCAGCTTCCTGCCTGTTACTCTCCACAGTATGCCGAAGAATATCCCTGACT
TCTAGCCCTGTGCGCCTTCTTTTGTCTGCTGTTGCTACTAATAGCCTTGGAGATCATGGTTGGTG

Exon2

GTCACCTCTCTTTGCTTCAACTTCACCTATAAAATCATTTGCCAGACCTGGACAGCCCTGGTGTGAAGGCGAGGTCTTCTTGA
ATAAAAATCTTTTCCTTCAGTACAACAGTGACAACAACATGGTCAAACTCTGGCCCTCCTGGGGAAGAAGGTATATGCCCA
CCAGCACCTTGGGGAGAATTGACCCAAACGCTGGGAGAAGTGGGGCGAGACCTCAGGATGCTCCTTTGTGACATCAAAACCCC
AGATAAAGACCAGT

Exon3

GATCCTTCCACTCTGCAAGTCGAGATGTTTGTCAACGTGAAGCAGAACGGTGCACTGGTGCATCCTGGCAGTTCGCCACC
AATGGAGAGAAATCCCTCCTCTTTGACGCAATGAACATGACCTGGACAGTAATTAATCATGAAGCCAGTAAAGATCAAGGAG
ACATGGAAAGAAAGACAGAGGGCTGGAAAAGTATTTCAAGGAAGCTCTCAAAAGGGAGACTGCGATCACTGGCTCAGGGAATTC
TTAGGGCACTGGGAGGCAATGCCAGAACCGACA

Exon4

GTGTACACAGTAAATGCTTCAGATATCCACTGGTCTTCTAGTCTACCAGATAGATGGATCATCCTGGGGGCATTCAATC
CTGTTAGTTTAAATGGGAATTGTTCTCATCTGTCTGTGGCAAAATGGTGAGTGGCAGGCTGCTCTGGCCCTTGAGG
ACGTCTTAGTCTGGTAAG GACTCAAGAGAGGTTGAATCATGGG

Fig. 1E

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1 - ACCATACAGTGAGGGTGAATGTGTACACGCCAGCTTCCTGCCTGTACTCTCCACAGT - 60
 61 - ATGCGAAGAAATATCCCTGACTTCTAGCCCTGTGCGCCTTCTTTTGTCTGCTGTGCTA - 120
 - M R R I S L T S S P V R L L L F L L L L
 121 - CTAATAGCCTTGGAGATCATGGTTGGTGGTCACTCTCTTTGCTTCAACTTCACTATAAAA - 180
 - L I A L E I M V G G H S L C F N F T I K
 181 - TCATTGTCCAGACCTGGACAGCCCTGGTGTGAAGCGCAGGTCTTCTTGAATAAAAATCTT - 240
 - S L S R P G Q P W C E A Q V F L N K N L
 241 - TTCCTTCAGTACAACAGTGACAACAACATGGTCAAACCTCTGGGCCTCCTGGGGAAGAAG - 300
 - F L Q Y N S D N N M V K P L G L L G K K
 301 - GTATATGCCACCGCACTTGGGGAGAATTGACCCAAACGCTGGGAGAAGTGGGGCGAGAC - 360
 - V Y A T S T W G E L T Q T L G E V G R D
 361 - CTCAGGATGCTCCTTTGTGACATCAAACCCAGATAAAGACCAGTGATCCTTCCACTCTG - 420
 - L R M L L C D I K P Q I K T S D P S T L
 421 - CAAGTCGAGATGTTTGTCAACGTGAAGCAGAACGGTGCACCTGGTGCATCCTGGCAGTTC - 480
 - Q V E M F C Q Q R E A E R C T G A S W Q F
 481 - GCCACCAATGGAGAGAAATCCCTCCTCTTTGACGCAATGAACATGACCTGGACAGTAATT - 540
 - A T N G E K S L L F D A M N M T W T V I
 541 - AATCATGAAGCCAGTAAGATCAAGGAGACATGGAAGAAAGACAGAGGGCTGGAAAAGTAT - 600
 - N H E A S K I K E T W K K D R G L E K Y
 601 - TTCAGGAAGCTCTCAAAGGGAGACTGGATCACTGGCTCAGGGAATTTTAGGGCACTGG - 660
 - F R K L S K G D C D H W L R E F L G H W
 661 - GAGGCAATGCCAGAACCGACAGTGTCAACCAGTAATGCTTCAGATATCCACTGGTCTTCT - 720
 - E A M P E P T V S P V N A S D I H W S S
 721 - TCTAGTCTACCAGATAGATGGATCATCCTGGGGGCATTCATCCTGTAGTTTAAATGGGA - 780
 - S S L P D R W I I L G A F I L L V L M G
 781 - ATTGTTCTCATCTGTGTGGTGGCAAAATGGTGGCAGGCTGGTCTCTGGCCCTTG - 840
 - I V L I C V W W Q N G E W Q A G L W P L
 841 - AGGACGTCTTAGTCTGGTAAGGACTCAAGAGAGGTGAATCATGGG - 885
 - R T S *

Fig. 1F

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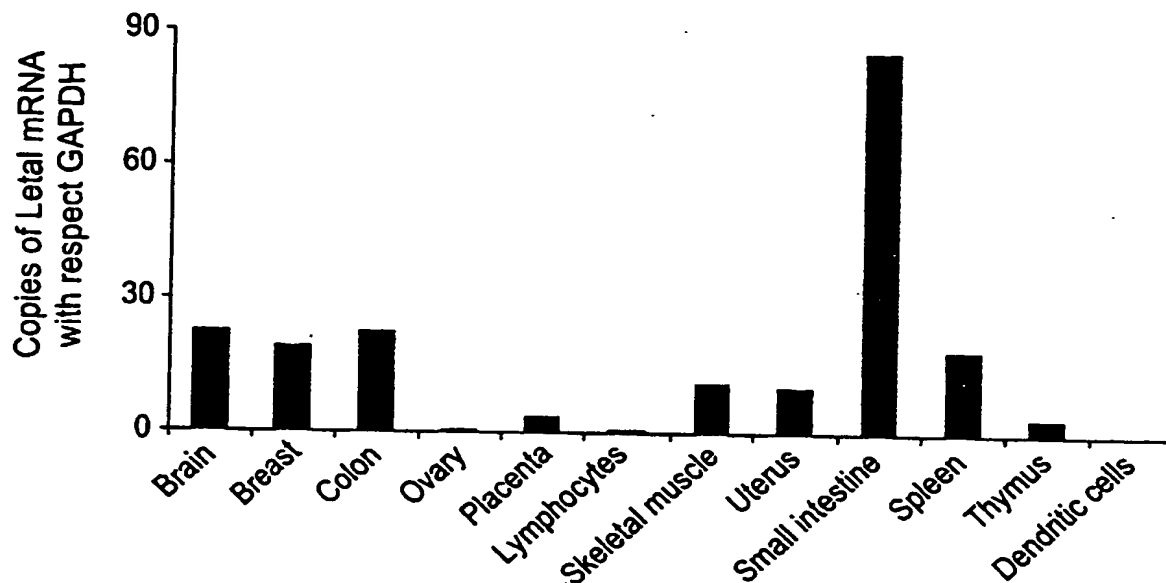


Fig. 2A

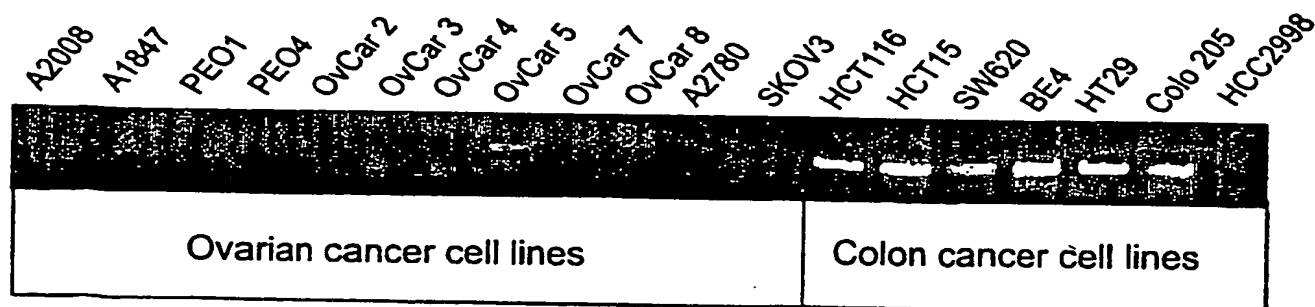


Fig. 2B

Fig. 3A

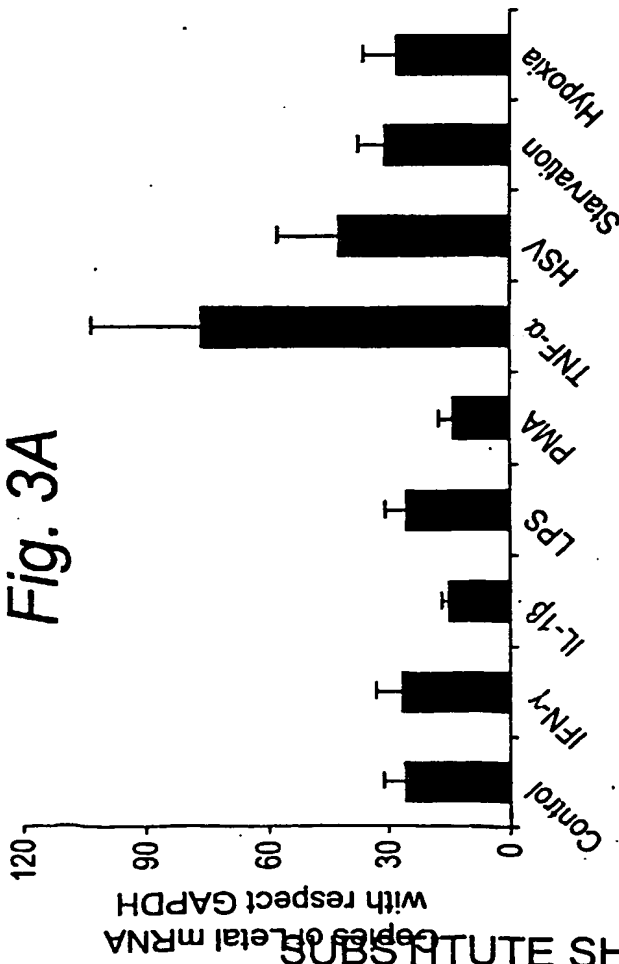
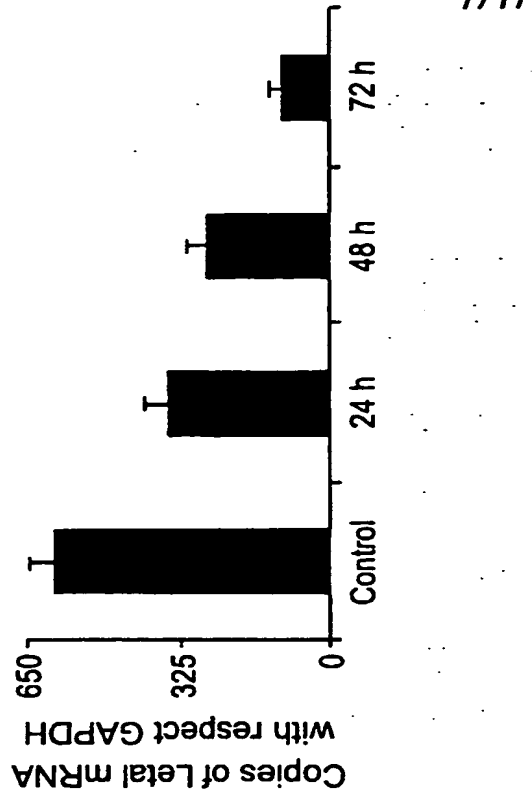


Fig. 3B



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Fig. 3C

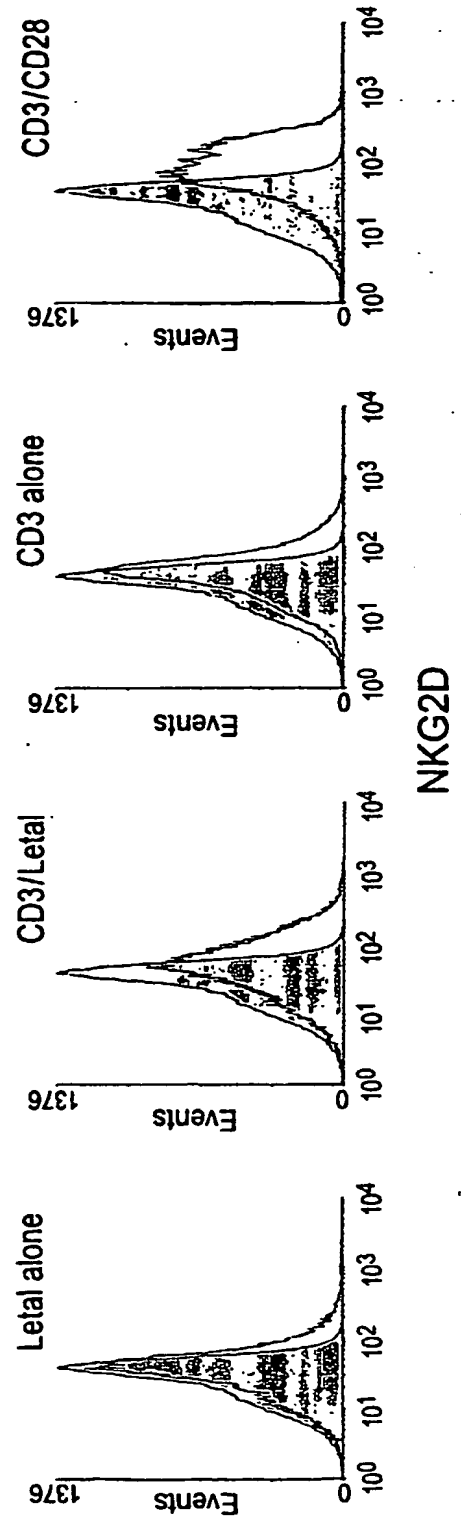


Fig. 4A

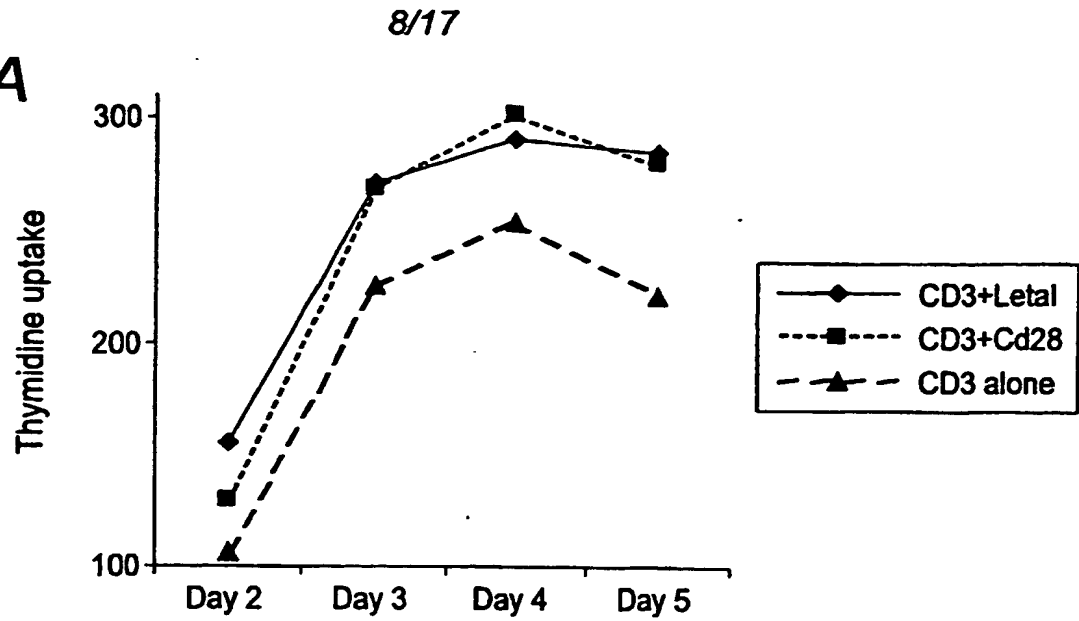


Fig. 4B

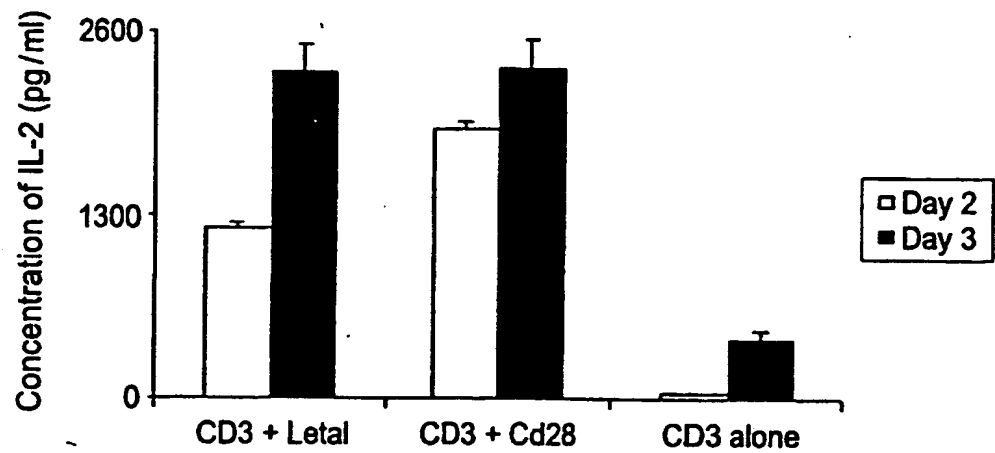
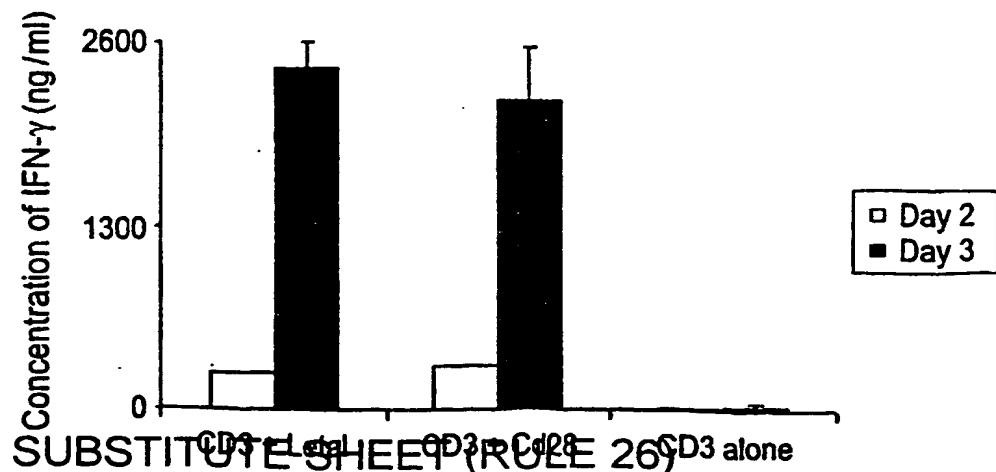


Fig. 4C



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Fig. 5A

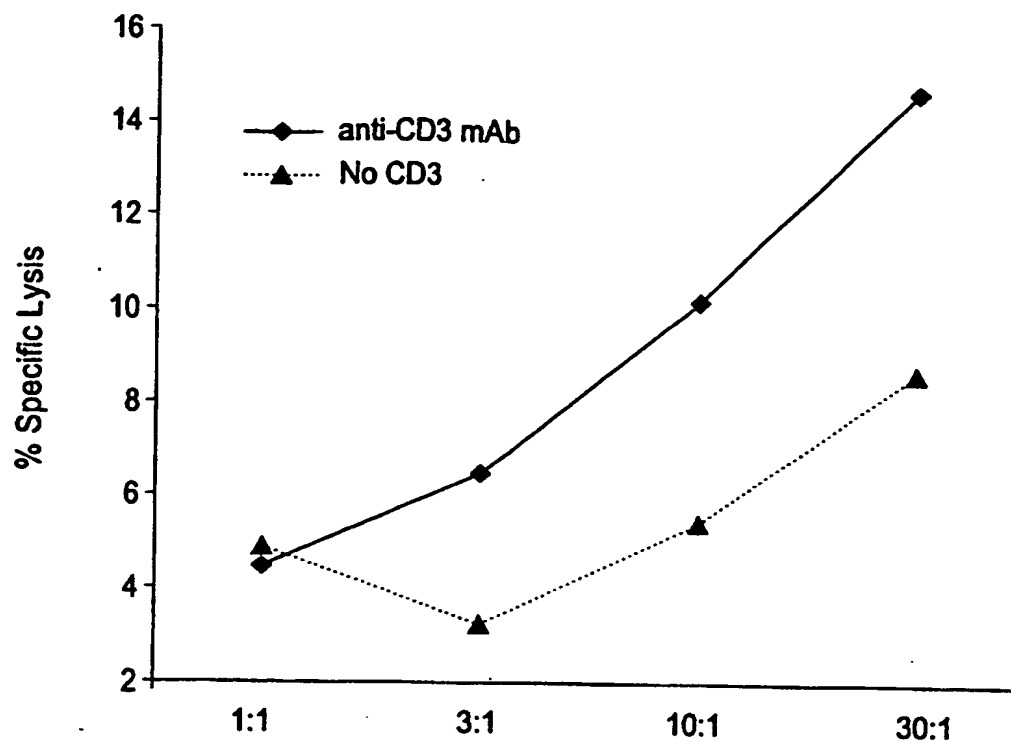
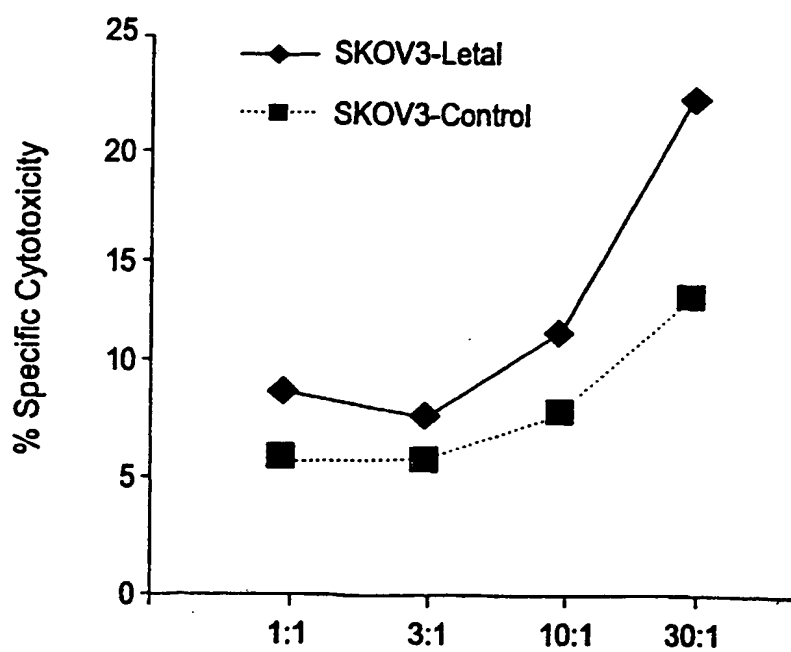
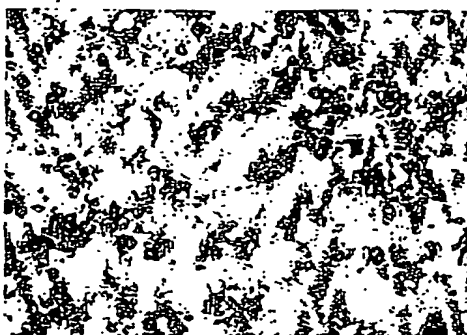
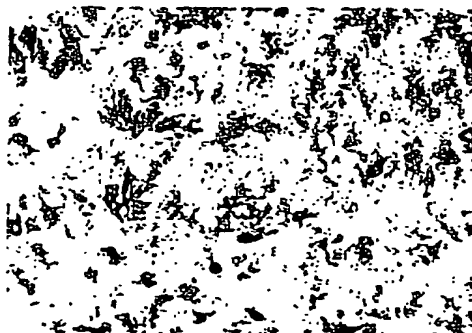
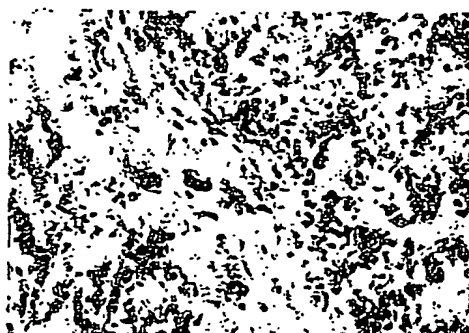
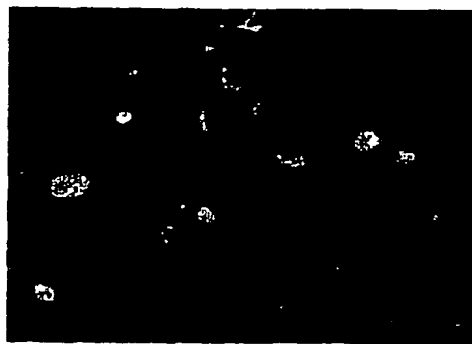
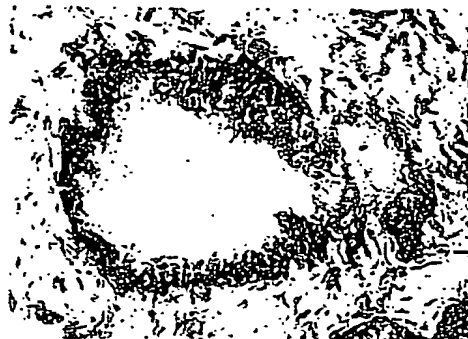


Fig. 5B



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Fig. 6A*Fig. 6B**Fig. 6C**Fig. 6D**Fig. 6E**Fig. 6F*

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Fig. 7A

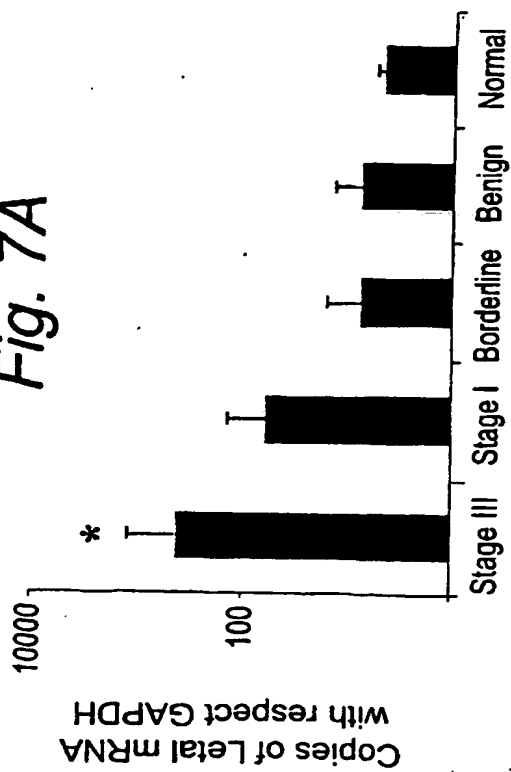


Fig. 7B

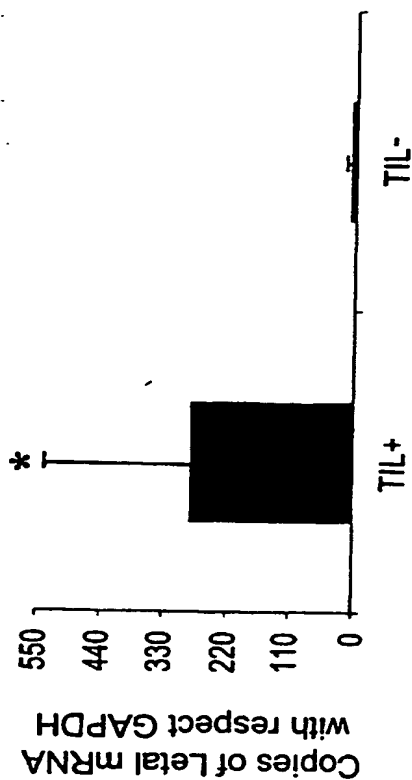


Fig. 7C

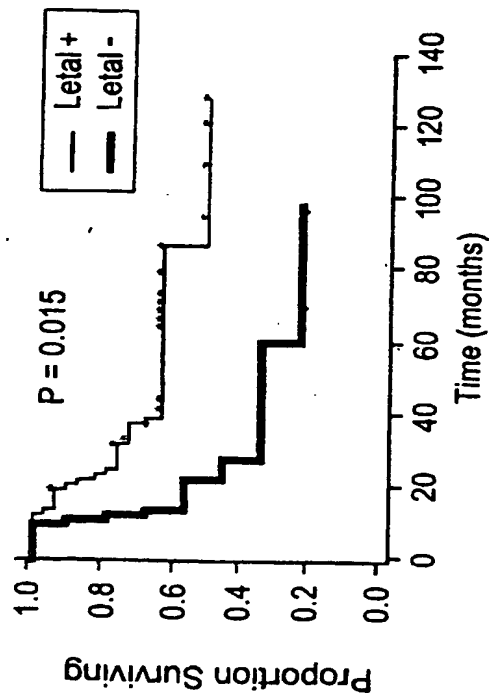
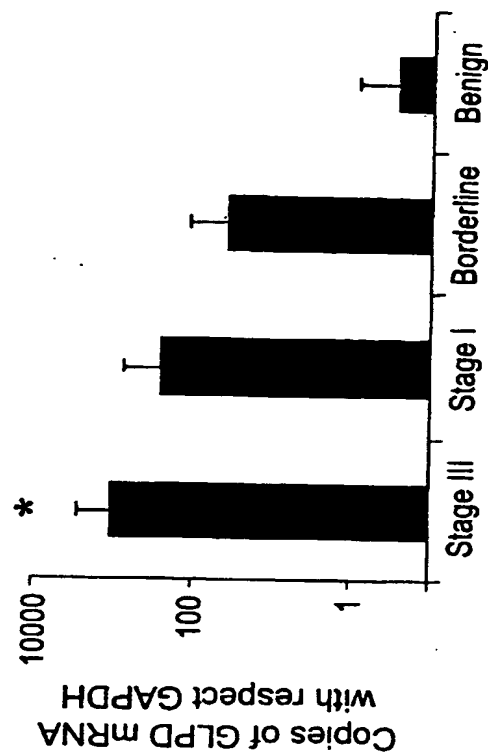


Fig. 7D



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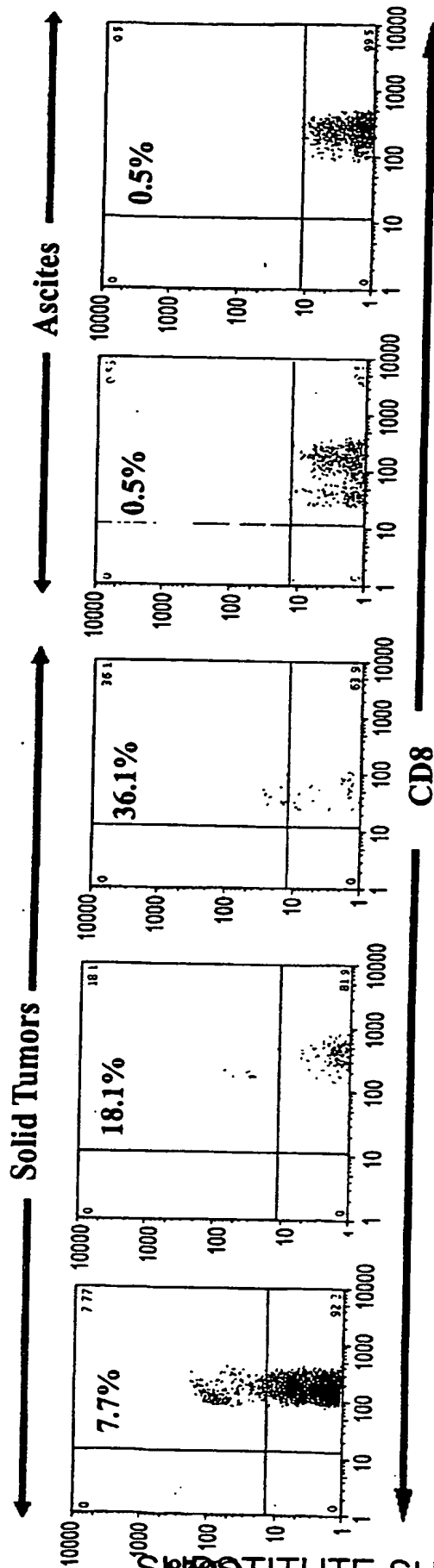


Fig. 8A

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Fig. 8B

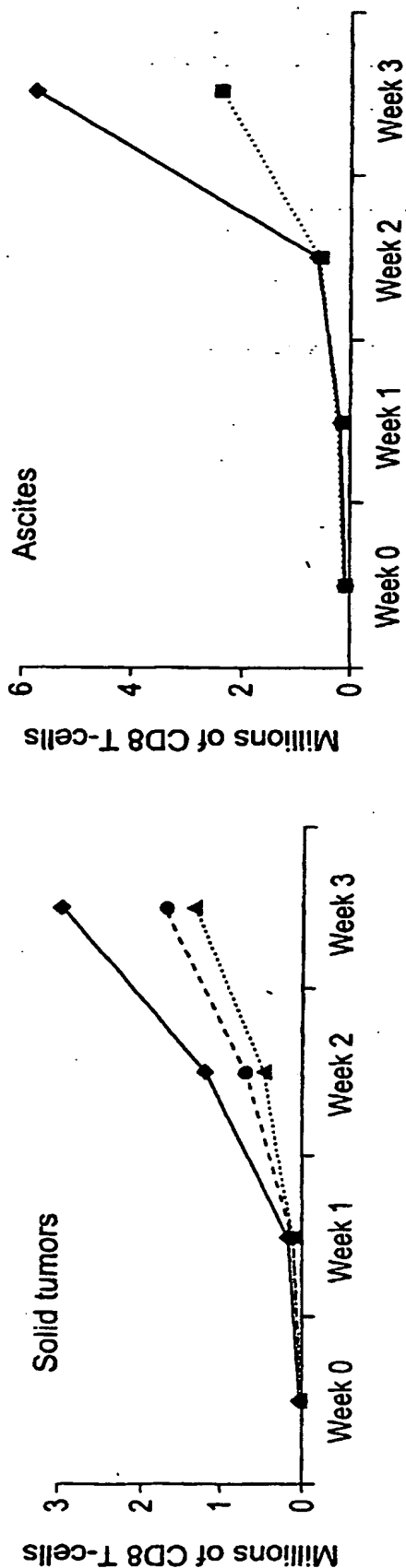
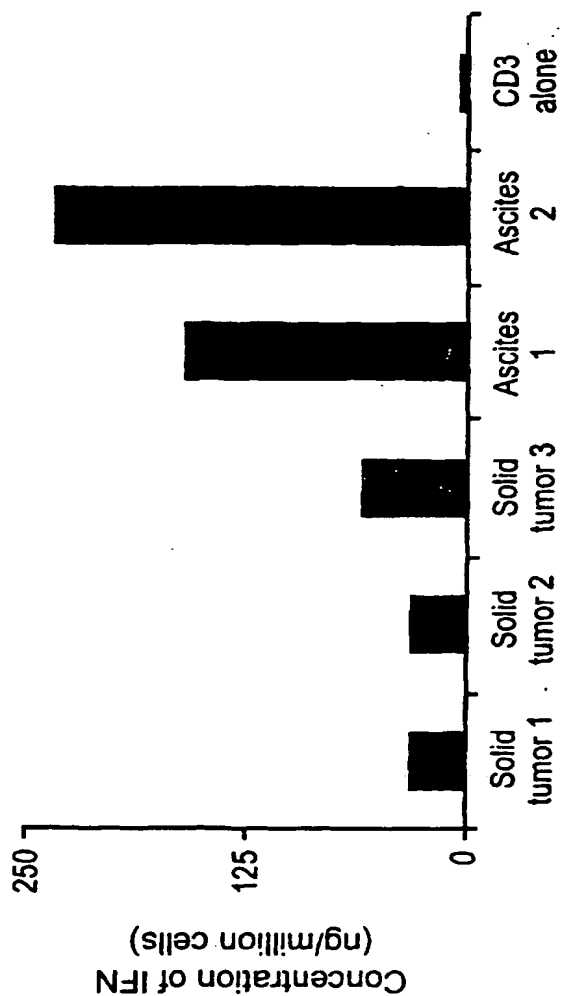


Fig. 8C



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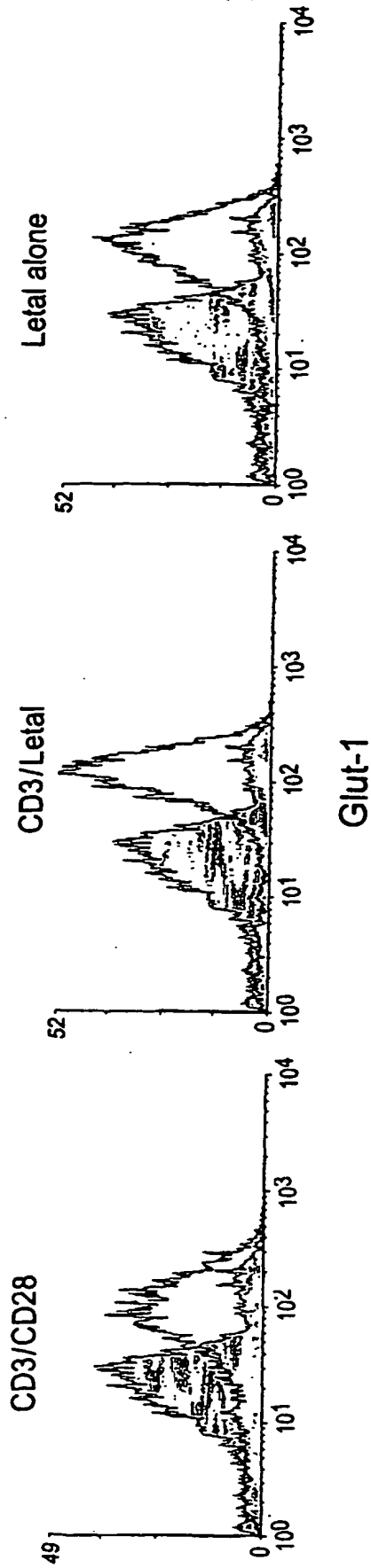


Fig. 9A

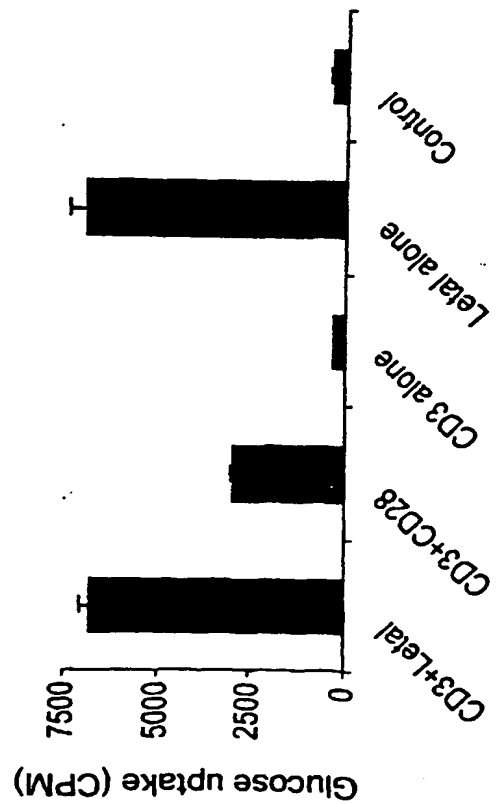


Fig. 9B

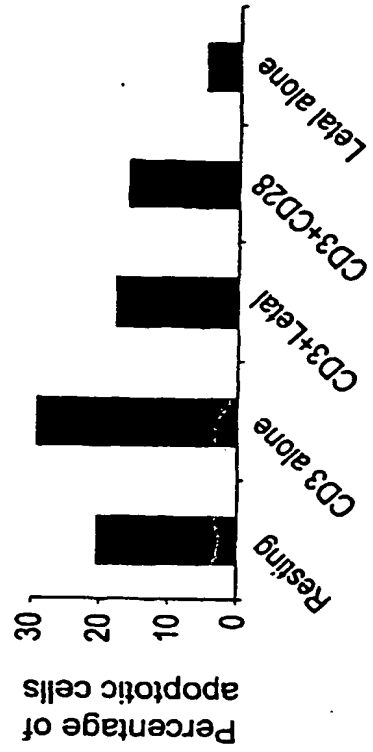


Fig. 9C

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Fig. 10A

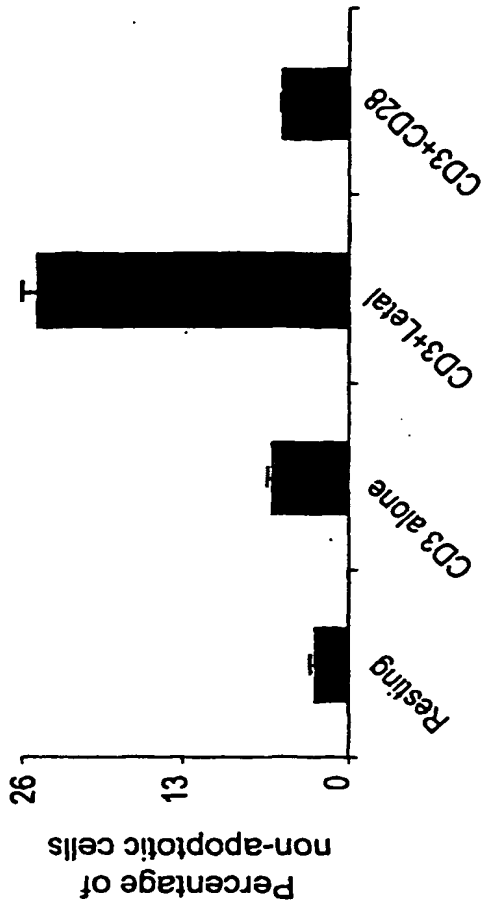
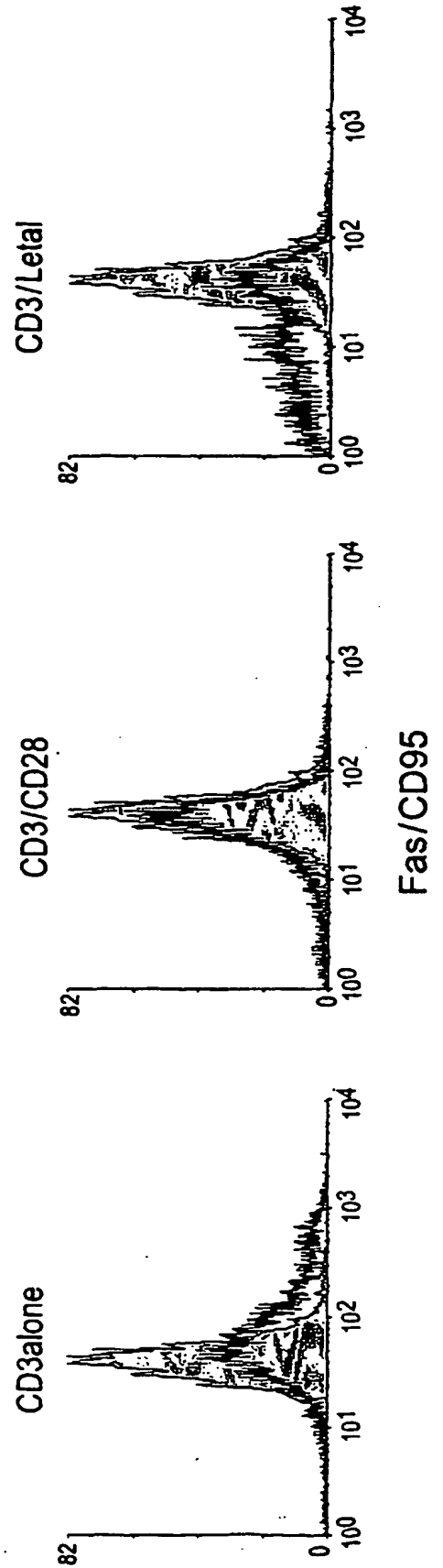


Fig. 10C

Fig. 10B



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TTTCGAGCACATGTGTTTTTATGAGAATTATGCTGAGATAGATTCTTTACATATTCATCAATGTC
TGAAGAAGTTACTTATGCAGATCTTCAATCCAGAACTCCAGTGAGATGGAAAAAATCCAGAAAT
TGGCAAAATTTGGGAAAAAGCACCTCCAGTCCCTCTCATGTATGGCGTCCAGCAGCCTTGTTTCT
GACTCTTCTGTGCCCTTCTGTGCTCATTTGGATTGGAGTCTTGGCAAGCATGTTTTCACGTAACTTT
GAAGATAGAAATGAAAAAATGAACAACTACAAACATCAGTGAAGAGCTCCAGAGAAATATTTTC
TCTACAACTGATGAGTAACATGAATATCTCCAACRAAGATCAGGAACCTCTCCACCACACTGCAAAAC
AATAGCCACCAAATTTATGTCGTGAGCTATATAGCAAGAACAGAGACAAATGTAGCCTTGTTCC
AAGGAGATGGATTTGGCATAAGGACAGCTGTTATTTCTTAAGTGATGATGTCCAAACATGGCAGGA
GAGTAAATGGCCTGTGCTGCTCAGAAATGCCAGCCTGTTGAAGATAAACAAACAAATGCATTGGA
ATTTATAAAATCCCAGAGTAGATCATATGACTATTGGCTGGGATTATCTCCTGAAGAAGATTCCAC
TCGTGATGAGAGTGGATAATAATAATCAACTCCTCTGCCCTGGTAAGTGT

Fig. 11

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1 - TTCGAGCACATGTGTTTTTATGAGAATTATGCTGAGATAGATTCTTTACATATTCATCA - 60
- M C F Y E N Y A E I D F F T Y S S
61 - ATGTCTGAAGAAGTTACTTATGCAGATCTTCAATCCAGAACTCCAGTGAGATGGAAAAA - 120
- M S E E V T Y A D L Q F Q N S S E M E K
121 - ATCCCAGAAATTGGCAAATTTGGGAAAAAGCACCTCCAGCTCCCTCTCATGTATGGCGT - 180
- I P E I G K F G E K A P P A P S H V W R
181 - CCAGCAGCCTTGTTCTGACTCTTCTGTGCCTTCTGTGCTCATTTGGAGTCTTG - 240
- P A A L F L T L L C L L L L I G L G V L
241 - GCAAGCATGTTTCACGTAACCTTTGAAGATAGAAAATGAACAACTACAAAC - 300
- A S M F H V T L K I E M K K M N K L Q N
301 - ATCAGTGAAGAGCTCCAGAGAAATATTTCTTACAACCTGATGAGTAACATGAATATCTCC - 360
- I S E E L Q R N I S L Q L M S N M N I S
361 - AACAAATCAGGAACCTCTCCACCACACTGCAACAATAAGCCACCAATATGTCGTGAG - 420
- N K I R N L S T T L Q T I A T K L C R E
421 - CTATATAGCAAGAACAAGAGCACAAATGTAAGCCTTGTCCAAGGAGATGGATTGGCAT - 480
- L Y S K E Q E H K C K P C P R R W I W H
481 - AAGGACAGCTGTTATTTCCCTAAGTATGATGTCCAAACATGGCAGGAGAGTAAATGGCC - 540
- K D S C Y F L S D D V Q T W Q E S K M A
541 - TGTGCTGCTCAGAAATGCCAGCCTGTTGAAGATAAACAACAATAATGCAATGGAATTATA - 600
- C A A Q N A S L L K I N N K N A L E F I
601 - AAATCCCAGAGTAGATCATATGACTATTGGCTGGGATTATCTCCTGAAGAAGATTCACCT - 660
- K S Q S R S Y D Y W L G L S P E E D S T
661 - CGTGGTATGAGAGTGGATAATAATCAACTCCTCTGCTGCTGTAAGTGT - 709
- R G M R V D N I I N S S A W *

Fig. 12

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